

Amendments to the Claims:

This listing of claims replaces all prior versions and listings of claims in the application:

Listing of Claims:

Claims 1-14. (Canceled)

Claim 15. (Currently amended) A method for identifying an agent that interacts with TNFR-1 DD, the method comprising ~~the steps of:~~

(a) determining an active site of TNFR-1 DD from a three dimensional structure of TNFR-1 DD; ~~and~~

(b) performing computer fitting analysis to identify an agent which interacts with said active site; and

obtaining the agent.

Claim 16. (Original) The method of Claim 15, wherein the active site is determined from the three dimensional structure model defined by the structural coordinates set forth in Figure 8,  $\pm$  a root mean square deviation from the conserved backbone atoms of said amino acids of not more than 1.5 Å.

Claim 17. (Original) The method of Claim 15, wherein the active site is characterized by a three dimensional structure comprising the relative structural coordinates of amino acid residues K343, E344, R347, R348 and D353 according to Figure 8,  $\pm$  a root mean square deviation from the conserved backbone atoms of said amino acids of not more than 1.5 Å.

Claim 18. (Original) The method of Claim 15, wherein the active site is characterized by a three dimensional structure comprising the relative structural coordinates of amino acid residues

E369 and Y373 according to Figure 8,  $\pm$  a root mean square deviation from the conserved backbone atoms of said amino acids of not more than 1.5 Å.

Claim 19. (Original) The method of Claim 15, wherein the active site is characterized by a three dimensional structure comprising the relative structural coordinates of amino acid residues E335, E386, E390, D398, E406, D407, E409 and E410 according to Figure 8,  $\pm$  a root mean square deviation from the conserved backbone atoms of said amino acids of not more than 1.5 Å.

Claim 20. (Original) The method of Claim 15, wherein the active site is characterized by a three dimensional structure comprising the relative structural coordinates of amino acid residues R358, R365, R368, R379, R380, R381, R384, R385, R394 and R397 according to Figure 8,  $\pm$  a root mean square deviation from the conserved backbone atoms of said amino acids of not more than 1.5 Å.

Claim 21. (Original) The method of Claim 15, further comprising contacting the identified agent with TNFR-1 DD in order to determine the effect the agent has on TNFR-1 DD.

Claim 22. (Original) The method of Claim 21, wherein the agent is an inhibitor of TNFR-1 DD.

Claim 23. (Original) The method of Claim 15, further comprising contacting the identified agent with TNFR-1 DD in the presence of a TNFR-1 DD binding molecule, and determining the effect the agent has on binding between TNFR-1 DD and the TNFR-1 DD binding molecule.

Claims 24-36. (Canceled)

Claim 37 (New). The method of claim 15, wherein obtaining the agent comprises synthesizing the agent.